

cons.aa	G G G V	A K	E
htGFER-II	LDLTVCKGRFAEVYKAKLKQNTSEQFETVAVKIFPYDHYASHDKDKDIFSDINLGHENILQF		
mActr-IIb	LLEIKARGRFCCVWKAQLKQ-----DFVAVKIKPLQDKQSWQSEREIFSTPGQGHENILQF		
mActr-II	LLEVKARGRFCCVWKAQLKQ-----EYVAVKIFPIQDKQSWQNEYEVYSIPGTGHENILQF		
daf-1	LKRVGSGRFQNVSRQDYRG-----EAVAVKVFRAIDEPAFHKEIEIFETRGLRHPHVLRY		
subdomains	I	II	III IV

htGFER-II	LTAEERKTELCKQYMLITAFKAKGNLQEYLTPKHVISWEDLRNVGSSSLARGLSKLPMSDHTP-C
mActr-IIb	IAAEFRGCSNLEVELMLITAFMDKQSLIDYLKGNIIITWNELOHVAETHSRGISYTLKHEDVPWCR
mActr-II	IGAEFRGTSVDVDAMLITAFHEKGSLSDFLKANVVSWNELCHIAETHARGGLAYLHEDIPLGL
daf-1	IGSDRVDTGFTELMLVIEYMPGSGLMDFLENTVNIETTYNLPASTASGLAFLENQIGGSK
subdomains	V VI-A

cons.aa	DLK N	DFG
htGFER-II	-GRPKQPIVGRDLVSSNIIWQDLTCCLDQFGLSLRL---CPYSSVDDLANSGQVGTARYMAP	
mActr-IIb	GECHUPSIAHGRDFKSKNVLLYSDLTAVLADFGLAVERF---EPGRFPQD--THCQVGTARYMAP	
mActr-II	-DCHKPAISGRDIYSKNVLLQRNLTAQIADFGALAKF---EAGYSAGD--THCQVGTARYMAP	
daf-1	-ESNKPAPQGRDIKSNTKTYQDLTCAIGDLGLSLSKPEDAASDIAN--ENYKCGTVRYLAP	
subdomains	VI-B	VII VIII

Fig. 1

a.a C C E G N M C
 5' GCGGATCCTGTTGTGAAGGNAATATGTG 3' Fig. 2A
 BAMHI C C G C

a.a V A V K I F
 5' GCGGATCCGTCGCAGTCAAAATTTT 3' Fig. 2B
 BamHI G C G G C
 T T T A

a.a R D I K S K N
 5' GCGGATCCGCGATATTAAAAGCAA 3' Fig. 2C
 BAMHI A C C GTCT
 G A

a.a E P A M Y
 5' CGGAATTCTCGTGCCATATA Fig. 2D
 EcoRI G G G
 A A

[illegible][illegible]

Fig. 3

[illegible]

- - - - - P Q D C P P D S - - - P L L C L - - - K P L Q L L L V K A R I C R A C R - 11
 - - - - - P Q D C P P D S - - - P V C L - - - K P L Q L L L K A R I C R A C R - 118
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R T E R - 11
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R T E R - 1 A R K - 5
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R A L K - 1
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R A L K - 2
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R A L K - 3
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R A L K - 4
 - - - - - P Q D C P P D S - - - P V C L - - - L P L Q L L L V C K R A L K - 6

Fig. 3 contd.

11

✓

v18

VIA

Fig. 3 contd.

K M N L T A C A D F G L A L K F E A G K S A C G D - - T H G Q V G T R R Y H N A P E V L E G A C R - I I
 K S O L T A V L A D F G L A V R F E P C K P P G D - - T H G Q V G T R R Y H N A P E V L E G A C R - I I
 K N D L T C C L D E G L S T R L D P T L S V D D L A N S Q V G T R R Y H N A P E V L D D T E R - I I
 X K G C C C A D L G L A V R H S Q S D Y L D I A P H R V G T K R Y M A P E V L D D T E R - I / A L K - 5
 K N G C C C I A D L G L A V M H S Q S T H Q L O V G M P R V G T K R Y M A P E V L D D T E R - I / A L K - 1
 K N G C C C I A D L G L A V K E M S D T N E V I D V G M P R V G T K R Y M A P E V L D D T E R - I / A L K - 2
 K N G C C C I A D L G L A V R H D A V T D I D I A P H R V G T K R Y M A P E V L D D T E R - I / A L K - 3
 K N G C C C I A D L G L A V R F I S D T N E V I D V G M P R V G T K R Y M A P E V L D D T E R - I / A L K - 4
 K N G C C C I A D L G L A V R F I S D T N E V I D V G M P R V G T K R Y M A P E V L D D T E R - I / A L K - 6

VII

VIII

A T M F Q R - D A F L R I O H Y A M G L V L W E L A S R C I T A A D C P P V D E Y M L P E E A C R - I I
 A L N F Q R - D A F L R I O H Y A M G L V L W E L V S R C K A A D C P P V D E Y M L P E E A C R - I I
 R M H L Q R A E S F R Q T O D Y A M G L V L W E M T S R C M A V - G E V K D Y E P P F G S T E R - I I
 S T R H K W F E S K R A D I Y A M G L V L W E I A R R T I V - G T H E D Y Q L P Y D T E R - I / A L K - 5
 Q I R T C C F S Y K R T O I M A F C L V L W E I A R R T I V - H G I V E D Y R P P F Y D A L K - 1
 T I Q V D C F S Y K R T O I M A F C L V L W E I A R R T I V - H G I V E D Y R P P F Y D A L K - 2
 S L R K N H F Q P Y I M A D I T S E G L T I W E M A R R C I T - G C I V E E Y Q L P Y D A L K - 3
 T L N M K H F D S F K C A D I Y A L L G L V W E I A R R C M S - G G V M E E Y Q L P Y D A L K - 4
 S L M R M H F Q S Y I M A D M Y S E G L T I W E I A R C I V S - G G I V E E Y Q L P Y H D A L K - 6

IX

X

E I G Q H P S L E D H Q E V V V H K K K R P V L R D Y M Q K H A G H A M L C E T I E C M A C R - I I
 E I G Q H P S L E L Q E V V V H K K K R P T T K O H M L K H P G I Q M V C E T I E C M A C R - I I
 K V R E H P S L E S H Q E V V V H K K K R P T T K O H M L K H P G I Q M V C E T I E C M A C R - I I
 L V P S O P S V E E M R K V V C E Q L R P N I P R M Q S C A C R V M A I M R E C M T E R - I / A L K - 5
 V V P M O P S V E E M R K V V C D Q Q T P T I P M R A A D P L S C A C R V M A I M R E C M A L K - 1
 V V P M O P S V E E M R K V V C D Q Q T P T I P M R A A D P L S C A C R V M A I M R E C M A L K - 2
 M V P S O P S V E E M R K V V C D Q Q T P T I P M R A A D P L S C A C R V M A I M R E C M A L K - 3
 L V P S O P S V E E M R K V V C D Q Q T P T I P M R A A D P L S C A C R V M A I M R E C M A L K - 4
 L V P S O P S V E E M R K V V C D Q Q T P T I P M R A A D P L S C A C R V M A I M R E C M A L K - 6

Fig. 3 contd.

18

PKESL (513) ACTR-II
 PKESI (536) ACTR-IIB
 K (567) YRR-II

Fig. 3 contd.

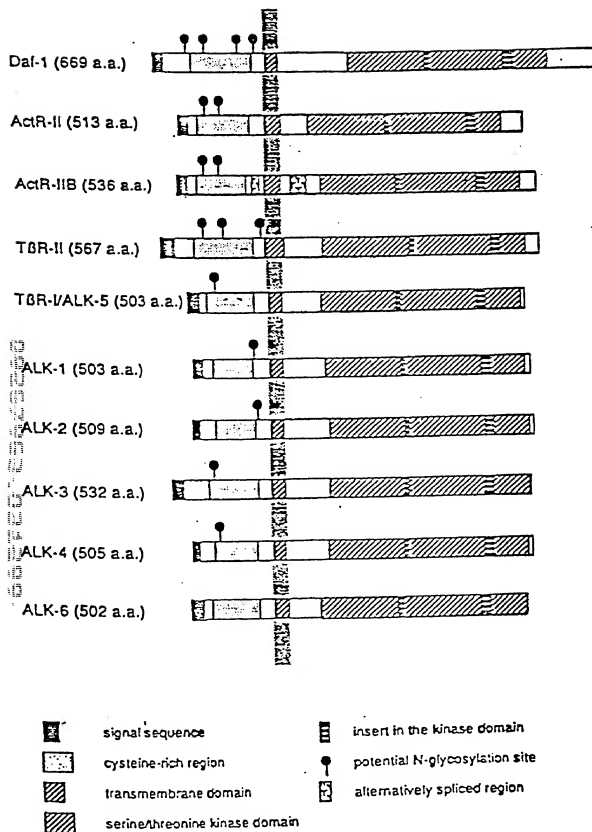


Fig. 4

C-F-----C-----CXGD-DI--TCET--G-CFVSL--SDG Majority
 T-----ESP-----HCKP-----TCR--GAHCTVVLVRFEC
 Y-----V-----CEGL-----CGNEDHCPGOCFSSLSINDDG
 A-----CISG-----PDD-AY-TCET--DGAACHVSVETTDALX-3/CR
 LFPN-----HHL-----CTXDA-NF-TCVAT-DGLLCFVSUETTDALX-4/CR
 ILYN-----ANWEDRTNQTGVEPCYGCCKKRRHCFAT--WKNI--SGTACR-11/CR
 CKR-----ANWELERTNOSGLERCEGECKKRLHCLYAS--WRNS--SGTACR-11/CR
 HCSREVCNARTTGWPGIEFLNETDRSFYENT--CTHDD-DSVQSA--RPSDNR-1/CR
 TEIVEKGC-----CYDRTL--GSPF-CVKSPKSPG-TVTEC-CEGDLC Majority
 RHPOEHRG-----REL-GRGRTE--FVNHXCDDSHLC
 FHVYOKGC-----GKMLT-C-GRPRPQOAV-EC-CGRDH
 GTTLASG-----GKMLT-C-GRPRPQOAV-EC-CGRDH
 HHHVVRTC-----IPKVEVPPAGKPFVCLSSSED-CYTDY
 KVTUHQGC-----IAEIDLIIPRDRLE-CPVCKKDPTE--WYFCCCKGNHC
 IELVKGCCWLDINGCYDRD-EDAAEKKCIHKKKPPGELFMCCSSSDFEC
 NLLRATVCHNDPKLPYHDFLEFHDTAACKVCTNNTNDPHECTWICCDKGNFC
 PRXSHFGC-----MDEKSVTDG

Fig. 5

ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TBR-II	dal-1	
79	60	61	63	40	40	37	39	ALK-1
	63	64	65	41	39	37	39	ALK-2
		63	65	41	38	37	39	ALK-3
			90	41	40	39	42	ALK-4
				42	40	41	43	ALK-5
					78	48	35	ActR-II
						47	32	ActR-IIB
							34	TBR-II

Fig. 6

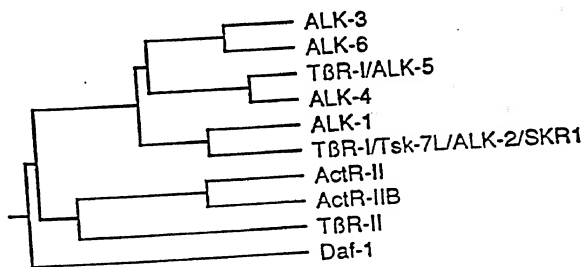


Fig. 7

FLAG-Smad5	-	+	+	+
c.a. ALK1-HA	-	-	+	-
c.a. ALK5-HA	-	-	-	+

IP : anti-FLAG
Blot : anti-phosphoserine

IP : anti-FLAG
Blot : anti-FLAG

IP : (-)
Blot : anti-HA

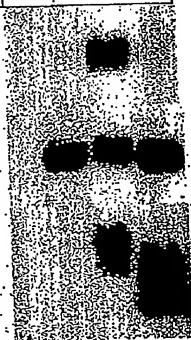


Fig. 8